AMENDMENTS TO THE CLAIMS

1. (previously presented) A method for identifying the phenotype of increased rib eye area in a *Bos taurus* animal, the method comprising:

   isolating a nucleic acid sample from the animal; and

   determining whether the animal has a T/C polymorphism present in the insulin-like growth factor 2 (*IGF2*) gene at position 150 of SEQ ID NO: 1;

   wherein the presence of a C residue (a C allele) at position 150 of SEQ ID NO : 1 is associated with the phenotype of increased rib eye area, as compared to an animal with a T residue (T allele) at position 150 of SEQ ID NO : 1.

2. (not entered) The method of Claim 1 wherein detecting the polymorphism comprises:

   isolating a genomic DNA sample from the animal;

   amplifying a region of the *Bos taurus IGF2* gene using an oligonucleotide pair to form nucleic acid amplification products comprising amplified *IGF2* gene polymorphism sequences;

   analyzing the amplification products to determine the presence or absence of the at least one C allele at position 150 of SEQ ID NO : 1.

3. (original) The method of Claim 2 wherein the oligonucleotide pair comprises SEQ ID NO: 2 and SEQ ID NO: 3.

4. (previously presented) The method of Claim 3 wherein the step of analyzing the amplification products comprises assessing whether they have a restriction fragment length polymorphism (RFLP).

5. (original) The method of Claim 4 wherein the RFLP is the presence or absence of a *BsrI* restriction site at nucleotide 150 in a nucleic acid amplification product

produced by amplification of a portion of the *IGF2* gene using the oligonucleotide pair SEQ ID NO: 2 and SEQ ID NO : 3.

6. (original) The method of Claim 2 further comprising the inclusion of a detectable moiety such that the amplification product comprises a labeled amplification product.

7. (original) The method of Claim 6 wherein the detectable moiety is selected from the group consisting of fluorescent, bioluminescent, chemiluminescent, radioactive and colorigenic moieties.

8. (previously presented) The method of Claim 2 further comprising:

contacting the nucleic acid amplification products with a hybridization probe;

wherein the hybridization probes comprise at least one oligonucleotide labeled with a detectable moiety;

under suitable conditions permitting hybridization of the at least one oligonucleotide to the amplification products to form a hybridization complex; and

wherein the presence of the detectable moiety in the hybridization complex indicates the presence of a *IGF2* polymorphism.

9. (previously presented) The method of Claim [2] wherein the nucleic acid amplification products are produced by an amplification method selected from the group of polymerase chain reaction (PCR), strand displacement amplification (SDA), nucleic acid sequence based amplification (NASBA), rolling circle amplification, T7 polymerase mediated amplification, T3 polymerase mediated amplification and SP6 polymerase mediated amplification.

10. (withdrawn) An isolated and purified nucleic acid comprising a portion of the bovine *IGF2* gene, further comprising a polymorphism at position 150 as defined by the positions in SEQ ID NO: 1, and in which there is a C residue or a T residue at position 150.

11. (previously presented) A method of sorting individual *Bos taurus* animals based on the knowledge of the animal's insulin-like growth factor 2 (*IGF2*) genotype, comprising the steps of:

determining whether the animal has C alleles or T alleles in the *IGF2* gene at position 150 of SEQ ID NO : 1;

wherein the genotype of the animal will be one of C/C, C/T, or T/T detected at position 150 of SEQ ID NO : 1; and

sorting the animals into groups of like genotype.

12. (withdrawn) A diagnostic kit for determining the *IGF2* genotype at position 150 of sequence ID NO: 1 in the *IGF2* gene of a bovine animal, the kit comprising:

oligonucleotide primers for amplifying a portion of the *IGF2* gene;

the primers comprising a forward primer comprising, at it's 3' end, sequence identical to at least 10 contiguous nucleotides within SEQ ID NO: 1;

a reverse primer comprising, at it's 3' end, a nucleotide sequence fully complementary to at least 10 contiguous nucleotides with SEQ ID NO: 1;

and wherein the forward and reverse primers will produce, in a PCR amplification reaction, a nucleic acid product amplification product containing a residue corresponding to position 150 of SEQ ID NO : 1.

13. (withdrawn) The kit of Claim 12 wherein the primers comprise the oligonucleotides SEQ ID NO: 2 and SEQ ID NO: 3.

14. (withdrawn) The kit of Claim 12 wherein the primers are labeled with a detectable moiety.

15. (withdrawn) The kit of Claim 12 further comprising at least one oligonucleotide, labeled with a detectable moiety and suitable for use as a hybridization probe.

Claims 16 to 19 (cancelled)

20. (not entered) A method for genotyping a *Bos taurus* animal comprising:

isolating a genomic DNA sample from the animal;

determining whether the animal has C residue (a C allele) or T residue (a T allele) in the insulin-like growth factor 2 (*IGF 2)* gene at position 150 of SEQ ID NO : 1,[[~~and~~]]

assigning either the C/C, C/T or T/T genotype, at position 150 of SEQ ID NO : 1, to the animal [[, and]]

wherein the C/C or C/T genotype is associated with increased rib-eye area as compared to the T/T genotype.

21. (previously presented) The method of Claim 20 wherein the step of determining comprises amplifying a region of the *Bos taurus IGF 2* gene in the isolated genomic DNA sample, using an oligonucleotide pair, to form nucleic acid amplification products comprising position 150 of SEQ ID NO : 1, and analyzing the amplification products to determine whether they have a C residue (a C allele) or T residue (a T allele).